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1 1. A method for detecting the presence of at least one selected strain of an organism
2 in a sample, comprising the steps of:

3 providing a sample that may comprise nucleic acid from at least one selected
4 strain of an organism and nucleic acid from at least one non-selected strain of the
5 organism;

6 providing a plurality of primers substantially complementary to regions of both
7 said nucleic acid from at least one selected strain of the organism and said nucleic acid
8 from at least one non-selected strain of the organism;

9 exposing said sample to at least one probe that is sufficiently complementary to a
10 portion of said nucleic acid from at least one non-selected strain to block full length
11 amplification of said nucleic acid from at least one non-selected strain between said
12 plurality of primers, said at least one probe comprising a nucleic acid analog;

13 amplifying said nucleic acid from at least one selected strain between said
14 plurality of primers; and

15 detecting amplification product of nucleic acid from at least one selected strain.

1 2. The method of claim 1, wherein said at least one selected strain comprises a
2 pathogenic strain.

1 3. The method of claim 2, wherein said sample is derived from a subject and said
2 pathogenic strain indicates a risk of cancerous growth in said subject.

1 4. The method of claim 1, wherein said organism comprises human papilloma virus
2 (HPV).

1 5. The method of claim 1, wherein said at least one probe comprises PNA.

1 6. The method of claim 5, wherein said at least one probe further comprises a
2 nucleotide different from PNA.

- 1 7. The method of claim 1, wherein each of said at least one probe comprises at least
2 8 bases.
- 1 8. The method of claim 1, wherein the step of amplifying said nucleic acid of at least
2 one selected strain between said plurality of primers comprises conducting a reaction
3 selected from the group consisting of a polymerase chain reaction, a ligase chain
4 reaction, a rolling circle replication, a branched chain amplification, a nucleic acid
5 based sequence amplification (NASBA), a Cleavase Fragment Length
6 Polymorphism, ICAN and RAM .
- 1 9. The method of claim 4, wherein said regions of both said nucleic acids are
2 parts of a region selected from the group consisting of L1, L2, E1, E6, and E7 region.
- 1 10. The method of claim 4, wherein said at least one non-selected strain equals
2 all the low-risk HPV strains known.
- 1 11. The method of claim 4, wherein said at least one non-selected strain is
2 selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.
- 1 12. The method of claim 4, wherein said at least one selected strain comprises a
2 plurality of high-risk HPV strains.
- 1 13. The method of claim 4, wherein said plurality of primers comprise MY09 and
2 MY11 (SEQ. ID. NOS. 10 and 11).
- 1 14. The method of claim 4, wherein said at least one probe is selected from the
2 group of sequences consisting of SEQ. ID. NO. 6 and SEQ. ID. NO. 7.
- 1 15. The method of claim 1, wherein said sample is a cervical scraping.
- 1 16. The method of claim 1, wherein said step of detecting amplification
2 product comprises in-gel electrophoresis of said product and staining said product
3 with ethidium bromide.

17-37. Canceled.